



PCT10

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/089,320

DATE: 04/24/2002  
TIME: 07:48:43

Input Set : A:\PTO.AMC.txt  
Output Set: N:\CRF3\04242002\J089320.raw

Does Not Comply  
Corrected Diskette Needed

4 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD.  
6 <120> TITLE OF INVENTION: Shear stress-responsive genes  
8 <130> FILE REFERENCE: PH-1064-PCT  
10 <140> CURRENT APPLICATION NUMBER: US/10/089,320  
12 <141> CURRENT FILING DATE: 2002-03-28  
14 <150> PRIOR APPLICATION NUMBER: JP 1999-280976  
16 <151> PRIOR FILING DATE: 1999-10-01  
18 <160> NUMBER OF SEQ ID NOS: 181  
20 <170> SOFTWARE: PatentIn Ver. 2.0

*pr 1-18*

## ERRORED SEQUENCES

1278 <210> SEQ ID NO: 7  
1280 <211> LENGTH: 2433 (p.3)  
1282 <212> TYPE: DNA  
1284 <213> ORGANISM: Homo sapiens  
1286 <220> FEATURE:  
1288 <221> NAME/KEY: CDS  
1290 <222> LOCATION: (214)..(1146)  
1292 <400> SEQUENCE: 7  
1294 atgccagccc caaacctcat ccotagtggg ggccttgctg atgtggaagt ggccagggcc 60  
1296 ctcatggtag gctgggcaga agcccaagaa caggctctaa agctgctaaa ccgggcagtc 120  
1298 ctgggtcccg gaggtcttg ccagtctgac agtgttcttg gcaactgctca aaggtccag 180  
1300 cagctggggt tccccgtcag cccgtgagcg gcc atg tcc aac ccc agc gcc cca 234  
1302 Met Ser Asn Pro Ser Ala Pro  
1304 1 5  
1306 cca cca tat gaa gac cgc aac ccc ctg tac cca ggc cct ccg ccc cct 282  
1308 Pro Pro Tyr Glu Asp Arg Asn Pro Leu Tyr Pro Gly Pro Pro Pro  
1310 10 15 20  
1312 ggg ggc tat ggg cag cca tct gtc ctg cca gga ggg tat cct gcc tac 330  
1314 Gly Gly Tyr Gly Gln Pro Ser Val Leu Pro Gly Gly Tyr Pro Ala Tyr  
1316 25 30 35  
1318 cct ggc tac ccg cag cct ggc tac ggt cac cct gct ggc tac cca cag 378  
1320 Pro Gly Tyr Pro Gln Pro Gly Tyr Gly His Pro Ala Gly Tyr Pro Gln  
1322 40 45 50 55  
1324 ccc atg ccc ccc acc cac ccg atg ccc atg aac tac ggc cca ggc cat 426  
1326 Pro Met Pro Pro Thr His Pro Met Pro Met Asn Tyr Gly Pro Gly His  
1328 60 65 70  
1330 ggc tat gat ggg gag gag aga gcg gtg agt gat agc ttc ggg cct gga 474  
1332 Gly Tyr Asp Gly Glu Glu Arg Ala Val Ser Asp Ser Phe Gly Pro Gly  
1334 75 80 85  
1336 gag tgg gat gac cgg aaa gtg cga cac act ttt atc cga aag gtt tac 522

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1338 Glu Trp Asp Asp Arg Lys Val Arg His Thr Phe Ile Arg Lys Val Tyr
1340          90          95          100
1342 tcc atc atc tcc gtg cag ctg ctc atc act gtg gcc atc att gct atc 570
1344 Ser Ile Ile Ser Val Gln Leu Leu Ile Thr Val Ala Ile Ile Ala Ile
1346      105      110      115
1348 ttc acc ttt gtg gaa cct gtc agc gcc ttt gtg agg aga aat gtg gct 618
1350 Phe Thr Phe Val Glu Pro Val Ser Ala Phe Val Arg Arg Asn Val Ala
1352 120          125          130          135
1354 gtc tac tac gtg tcc tat gct gtc ttc gtt gtc acc tac ctg atc ctt 666
1356 Val Tyr Tyr Val Ser Tyr Ala Val Phe Val Val Thr Tyr Leu Ile Leu
1358          140          145          150
1360 gcc tgc tgc cag gga ccc aga cgc cgt ttc cca tgg aac atc att ctg 714
1362 Ala Cys Cys Gln Gly Pro Arg Arg Arg Phe Pro Trp Asn Ile Ile Leu
1364          155          160          165
1366 ctg acc ctt ttt act ttt gcc atg ggc ttc atg acg ggc acc att tcc 762
1368 Leu Thr Leu Phe Thr Phe Ala Met Gly Phe Met Thr Gly Thr Ile Ser
1370          170          175          180
1372 agt atg tac caa acc aaa gcc gtc atc att gca atg atc atc act gcg 810
1374 Ser Met Tyr Gln Thr Lys Ala Val Ile Ile Ala Met Ile Ile Thr Ala
1376      185      190      195
1378 gtg gta tcc att tca gtc acc atc ttc tgc ttt cag acc aag gtg gac 858
1380 Val Val Ser Ile Ser Val Thr Ile Phe Cys Phe Gln Thr Lys Val Asp
1382 200          205          210          215
1384 ttc acc tcg tgc aca ggc ctc ttc tgt gtc ctg gga att gtg ctc ctg 906
1386 Phe Thr Ser Cys Thr Gly Leu Phe Cys Val Leu Gly Ile Val Leu Leu
1388          220          225          230
1390 gtg act ggg att gtc act agc att gtg ctc tac ttc caa tac gtt tac 954
1392 Val Thr Gly Ile Val Thr Ser Ile Val Leu Tyr Phe Gln Tyr Val Tyr
1394          235          240          245
1396 tgg ctc cac atg ctc tat gct gct ctg ggg gcc att tgt ttc acc ctg 1002
1398 Trp Leu His Met Leu Tyr Ala Ala Leu Gly Ala Ile Cys Phe Thr Leu
1400          250          255          260
1402 ttc ctg gct tac gac aca cag ctg gtc ctg ggg aac cgg aag cac acc 1050
1404 Phe Leu Ala Tyr Asp Thr Gln Leu Val Leu Gly Asn Arg Lys His Thr
1406          265          270          275
1408 atc agc ccc gag gac tac atc act ggc gcc ctg cag att tac aca gac 1098
1410 Ile Ser Pro Glu Asp Tyr Ile Thr Gly Ala Leu Gln Ile Tyr Thr Asp
1412 280          285          290          295
1414 atc atc tac atc ttc acc ttt gtg ctg cag ctg atg ggg gat cgc aat 1146
1416 Ile Ile Tyr Ile Phe Thr Phe Val Leu Gln Leu Met Gly Asp Arg Asn
1418          300          305          310
1420 taaggagcaa gccccattt tcaccgacg ctgggctctc ccttccaagc tagagggtg 1206
1422 ggccctatga ctgtggtctg ggcttttaggc ccctttcctt ccccttgagt aacatgccca 1266
1424 gtttccttct tgctcctggag acaggtggcc tctctggcta tggatgtgtg ggtacttggt 1326
1426 ggggacggag gagctaggga ctaactgttg ctcttggttg gcttggcagg gactaggctg 1386
1428 aagatgtgtc ttctccccgc cacctactgt atgacaccac attcttccta acagctgggg 1446
1430 ttgtgaggaa tatgaaaaga gcctattcga tagctagaag ggaatatgaa aggtagaagt 1506
1432 gacttcaagg tcacgaggtt cccctcccac ctctgtcaca ggcttcttga ctacgtagtt 1566
1434 ggagctatatt ctccccccag caaagccaga gagctttgtc cccggcctcc tggacacata 1626

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1436 ggccattatc ctgtattcct ttggttggc atcttttagc tcaggaaggt agaagagatc 1686
1438 tgtgcccatt ggtctccttg cttcaatccc ttctgttttc agtgacatat gtattgttta 1746
1440 tctgggtag ggatggggga cagataatag aacgagcaaa gtaacctata caggccagca 1806
1442 tggaacagca tctcccctgg gcttgctcct ggcttgtgac gctataagac agagcaggcc 1866
1444 acatgtggcc atctgctccc cattcttgaa agctgctggg gcctccttgc aggtcttctgg 1926
1446 atctctggtc agagtgaact cttgcttcct gtattcaggc agctcagagc agaaagtaag 1986
1448 gggcagagtc atacgtgtgg ccaggaagta gccagggtga agagagactc ggtgcccga 2046
1450 gggagaatgc ctgggggtcc ctcacctggc tagggagata ccgaagccta ctgtggtact 2106
1452 gaagacttct gggttcttct cttctgctaa cccagggagg gtcctaagag gaaggtgact 2166
1454 tctctctgtt tgtcttaagt tgcactgggg gatttctgac ttgaggccca tctctccagc 2226
1456 cagccactgc cttctttgta atattaagt ccttgagctg gaatggggaa gggggacaag 2286
1458 ggtcagctcg tcgggtgggg gcagaaatca aatcagccca aggatatagt taggattaat 2346
1460 tacttaatat agaaatccta actatatcac acaaagggat acaactataa atgtaataaa 2406

```

E--&gt; 1462 atttatgtct agaagtt

2423

17629 &lt;210&gt; SEQ ID NO: 88

17631 &lt;211&gt; LENGTH: 402

17633 &lt;212&gt; TYPE: PRT

17635 &lt;213&gt; ORGANISM: Homo sapiens

17637 &lt;400&gt; SEQUENCE: 88

17639 Met Gln Met Ser Pro Ala Leu Thr Cys Leu Val Leu Gly Leu Ala Leu

E--&gt; 17641 Val Phe Gly Glu Gly Ser Ala Val His His Pro Pro Ser Tyr Val Ala

17643 1 5 10 15

17645 His Leu Ala Ser Asp Phe Gly Val Arg Val Phe Gln Gln Val Ala Gln

17647 20 25 30

17649 Ala Ser Lys Asp Arg Asn Val Val Phe Ser Pro Tyr Gly Val Ala Ser

17651 35 40 45

17653 Val Leu Ala Met Leu Gln Leu Thr Thr Gly Gly Glu Thr Gln Gln Gln

17655 50 55 60

17657 Ile Gln Ala Ala Met Gly Phe Lys Ile Asp Asp Lys Gly Met Ala Pro

17659 65 70 75 80

17661 Ala Leu Arg His Leu Tyr Lys Glu Leu Met Gly Pro Trp Asn Lys Asp

17663 85 90 95

17665 Glu Ile Ser Thr Asp Ala Ile Phe Val Gln Arg Asp Leu Lys Leu

17667 100 105 110

17669 Val Gln Gly Phe Met Pro His Phe Phe Arg Leu Phe Arg Ser Thr Val

17671 115 120 125

17673 Lys Gln Val Asp Phe Ser Glu Val Glu Arg Ala Arg Phe Ile Ile Asn

17675 130 135 140

17677 Asp Trp Val Lys Thr His Thr Lys Gly Met Ile Ser Asn Leu Leu Gly

17679 145 150 155 160

17681 Lys Gly Ala Val Asp Gln Leu Thr Arg Leu Val Leu Val Asn Ala Leu

17683 165 170 175

17685 Tyr Phe Asn Gly Gln Trp Lys Thr Pro Phe Pro Asp Ser Ser Thr His

17687 180 185 190

17689 Arg Arg Leu Phe His Lys Ser Asp Gly Ser Thr Val Ser Val Pro Met

17691 195 200 205

17693 Met Ala Gln Thr Asn Lys Phe Asn Tyr Thr Glu Phe Thr Thr Pro Asp

17695 210 215 220

17697 Gly His Tyr Tyr Asp Ile Leu Glu Leu Pro Tyr His Gly Asp Thr Leu

There  
belong  
under  
amino acids  
in first  
line.

Please  
re-number  
all amino  
acids in  
seq: 88

## RAW SEQUENCE LISTING

DATE: 04/24/2002

PATENT APPLICATION: US/10/089,320

TIME: 07:48:45

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\04242002\J089320.raw

```

17699 225          230          235          240
17701 Ser Met Phe Ile Ala Ala Pro Tyr Glu Lys Glu Val Pro Leu Ser Ala
17703          245          250          255
17705 Leu Thr Asn Ile Leu Ser Ala Gln Leu Ile Ser His Trp Lys Gly Asn
17707          260          265          270
17709 Met Thr Arg Leu Pro Arg Leu Leu Val Leu Pro Lys Phe Ser Leu Glu
17711          275          280          285
17713 Thr Glu Val Asp Leu Arg Lys Pro Leu Glu Asn Leu Gly Met Thr Asp
17715          290          295          300
17717 Met Phe Arg Gln Phe Gln Ala Asp Phe Thr Ser Leu Ser Asp Gln Glu
17719 305          310          315          320
17721 Pro Leu His Val Ala Gln Ala Leu Gln Lys Val Lys Ile Glu Val Asn
17723          325          330          335
17725 Glu Ser Gly Thr Val Ala Ser Ser Ser Thr Ala Val Ile Val Ser Ala
17727          340          345          350
17729 Arg Met Ala Pro Glu Glu Ile Ile Met Asp Arg Pro Phe Leu Phe Val
17731          355          360          365
17733 Val Arg His Asn Pro Thr Gly Thr Val Leu Phe Met Gly Gln Val Met
17735          370          375          380
17737 Glu Pro
17739 385
18363 <210> SEQ ID NO: 94
18365 <211> LENGTH: 99
18367 <212> TYPE: PRT
18369 <213> ORGANISM: Homo sapiens
18371 <400> SEQUENCE: 94
18373 Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala Phe Leu Ile Ser
E--> 18375 Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser Ala Lys Glu Leu
18377 1 5 10 15
18379 Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe His Pro Lys Phe
18381          20          25          30
18383 Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr
18385          35          40          45
18387 Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu Cys Leu Asp Pro
18389          50          55          60
18391 Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys Phe Leu Lys Arg Ala
18393 65          70          75          80
18395 Glu Asn Ser
21291 <210> SEQ ID NO: 110
21293 <211> LENGTH: 534
21295 <212> TYPE: PRT
21297 <213> ORGANISM: Homo sapiens
21299 <400> SEQUENCE: 110
21301 Met Phe Ser Trp Val Ser Lys Asp Ala Arg Arg Lys Lys Glu Pro Glu
21303 1 5 10 15
21305 Leu Phe Gln Thr Val Ala Glu Gly Leu Arg Gln Leu Tyr Ala Gln Lys
21307          20          25          30
21309 Leu Leu Pro Leu Glu Glu His Tyr Arg Phe His Glu Phe His Ser Pro
21311          35          40          45

```

same  
error

re-number  
all amino  
acids

P.5

RAW SEQUENCE LISTING  
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DATE: 04/24/2002  
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Input Set : A:\PTO.AMC.txt  
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E--> 21313 Xaa Leu Glu Asp Ala Asp Phe Asp Asn Lys Pro Met Val Leu Leu Val  
 21315 50 55 60  
 E--> 21317 Xaa Gln Tyr Ser Thr Gly Lys Thr Thr Phe Ile Arg His Leu Ile Glu  
 21319 65 70 75 80  
 21321 Gln Asp Phe Pro Gly Met Arg Ile Gly Pro Glu Pro Thr Thr Asp Ser  
 21323 85 90 95  
 21325 Phe Ile Ala Val Met His Gly Pro Thr Glu Gly Val Val Pro Gly Asn  
 21327 100 105 110  
 21329 Ala Leu Val Val Asp Pro Arg Arg Pro Phe Arg Lys Leu Asn Ala Phe  
 21331 115 120 125  
 21333 Gly Asn Ala Phe Leu Asn Arg Phe Met Cys Ala Gln Leu Pro Asn Pro  
 21335 130 135 140  
 21337 Val Leu Asp Ser Ile Ser Ile Ile Asp Thr Pro Gly Ile Leu Ser Gly  
 21339 145 150 155 160  
 21341 Glu Lys Gln Arg Ile Ser Arg Gly Tyr Asp Phe Ala Ala Val Leu Glu  
 21343 165 170 175  
 21345 Trp Phe Ala Glu Arg Val Asp Arg Ile Ile Leu Leu Phe Asp Ala His  
 21347 180 185 190  
 21349 Lys Leu Asp Ile Ser Asp Glu Phe Ser Glu Val Ile Lys Ala Leu Lys  
 21351 195 200 205  
 21353 Asn His Glu Asp Lys Ile Arg Val Val Leu Asn Lys Ala Asp Gln Ile  
 21355 210 215 220  
 21357 Glu Thr Gln Gln Leu Met Arg Val Tyr Gly Ala Leu Met Trp Ser Leu  
 21359 225 230 235 240  
 21361 Gly Lys Ile Ile Asn Thr Pro Glu Val Val Arg Val Tyr Ile Gly Ser  
 21363 245 250 255  
 21365 Phe Trp Ser His Pro Leu Leu Ile Pro Asp Asn Arg Lys Leu Phe Glu  
 21367 260 265 270  
 21369 Ala Glu Glu Gln Asp Leu Phe Lys Asp Ile Gln Ser Leu Pro Arg Asn  
 21371 275 280 285  
 21373 Ala Ala Leu Arg Lys Leu Asn Asp Leu Ile Lys Arg Ala Arg Leu Ala  
 21375 290 295 300  
 21377 Lys Val His Ala Tyr Ile Ile Ser Ser Leu Lys Lys Glu Met Pro Asn  
 21379 305 310 315 320  
 21381 Val Phe Gly Lys Glu Ser Lys Lys Lys Glu Leu Val Asn Asn Leu Gly  
 21383 325 330 335  
 21385 Glu Ile Tyr Gln Lys Ile Glu Arg Glu His Gln Ile Ser Pro Gly Asp  
 21387 340 345 350  
 21389 Phe Pro Ser Leu Arg Lys Met Gln Glu Leu Leu Gln Thr Gln Asp Phe  
 21391 355 360 365  
 21393 Ser Lys Phe Gln Ala Leu Lys Pro Lys Leu Leu Asp Thr Val Asp Asp  
 21395 370 375 380  
 21397 Met Leu Ala Asn Asp Ile Ala Arg Leu Met Val Met Val Arg Gln Glu  
 21399 385 390 395 400  
 21401 Glu Ser Leu Met Pro Ser Gln Val Val Lys Gly Gly Ala Phe Asp Gly  
 21403 405 410 415  
 21405 Thr Met Asn Gly Pro Phe Gly His Gly Tyr Gly Glu Gly Ala Gly Glu  
 21407 420 425 430  
 21409 Gly Ile His Asp Val Glu Trp Val Val Gly Lys Asp Lys Pro Thr Tyr

*see  
 item 9  
 on Encl  
 Summary  
 sheet*

DATE: 04/24/2002  
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Input Set : A:\PTO.AMC.txt  
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[illegible]

edit  
globally

520 525

IMPORTANT: all bases  
must be in  
lower-case letters

also, see item 1

on End  
Summary  
Sheet

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```

E--> 27369  aga aaa ctt tta gac cat tta caa ttg gat aaa gtt cat ctt ttt ggc
      27370 459
      27371  Arg Lys Leu Leu Asp His Leu Gln Leu Asp Lys Val His Leu Phe Gly
      27372              95                      100                      105
E--> 27374  gct tct ttg gga ggc ttt ttg gcc cag aaa ttt gct gaa tat act cac
      27375 507
      27376  Ala Ser Leu Gly Gly Phe Leu Ala Gln Lys Phe Ala Glu Tyr Thr His
      27377              110                      115                      120
E--> 27379  aaa tct cct aga gtc cat tcc cta atc ctc tgc aat tcc ttc agt gac
      27380 555
      27381  Lys Ser Pro Arg Val His Ser Leu Ile Leu Cys Asn Ser Phe Ser Asp
      27382              125                      130                      135
E--> 27384  acc tct atc ttc aac caa act tgg act gca aac agc ttt tgg ctg atg
      27385 603
      27386  Thr Ser Ile Phe Asn Gln Thr Trp Thr Ala Asn Ser Phe Trp Leu Met
      27387 140                      145                      150                      155
E--> 27389  cct gca ttt atg ctc aaa aaa ata gtt ctt gga aat ttt tca tct ggc
      27390 651
      27391  Pro Ala Phe Met Leu Lys Lys Ile Val Leu Gly Asn Phe Ser Ser Gly
      27392              160                      165                      170
E--> 27394  ccg gtg gac cct atg atg gct gat gcc att gat ttc atg gta gac agg
      27395 699
      27396  Pro Val Asp Pro Met Met Ala Asp Ala Ile Asp Phe Met Val Asp Arg
      27397              175                      180                      185
E--> 27399  cta gaa agt ttg ggt cag agt gaa ctg gct tca aga ctt acc ttg aat
      27400 747
      27401  Leu Glu Ser Leu Gly Gln Ser Glu Leu Ala Ser Arg Leu Thr Leu Asn
      27402              190                      195                      200
E--> 27404  tgt caa aat tct tat gtg gta cct cat aaa att cgg gac ata cct gta
      27405 795
      27406  Cys Gln Asn Ser Tyr Val Val Pro His Lys Ile Arg Asp Ile Pro Val
      27407 205                      210                      215
E--> 27409  act att atg gat gtg ttt gat cag agt gcg ctt tca act gaa gct aaa
      27410 843
      27411  Thr Ile Met Asp Val Phe Asp Gln Ser Ala Leu Ser Thr Glu Ala Lys
      27412 220                      225                      230                      235
E--> 27414  gaa gaa atg tac aag ctg tat cct aat gcc cga aga gct cat ctg aaa
      27415 891
      27416  Glu Glu Met Tyr Lys Leu Tyr Pro Asn Ala Arg Arg Ala His Leu Lys
      27417              240                      245                      250
E--> 27419  aca gga ggc aat ttc cca tac ctg tgc aga agt gca gag gtc aat ctt
      27420 939
      27421  Thr Gly Gly Asn Phe Pro Tyr Leu Cys Arg Ser Ala Glu Val Asn Leu
      27422              255                      260                      265
E--> 27424  tat gta cag ata cat ttg ctg caa ttc cat gga acc aaa tac gcg gcc
      27425 987
      27426  Tyr Val Gln Ile His Leu Leu Gln Phe His Gly Thr Lys Tyr Ala Ala
      27427              270                      275                      280
E--> 27429  att gac cca tca atg gtc agt gcc gag gag ctt gag gtg cag aaa ggc

```

*same  
eval*

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27430 1035  
 27431 Ile Asp Pro Ser Met Val Ser Ala Glu Glu Leu Glu Val Gln Lys Gly  
 27432 285 290 295  
 E--> 27434 agc ctt ggc atc agc cag gag gag cag tagtgtgtct ctgctgtca  
 27435 atgatga 1089  
 27436 Ser Leu Gly Ile Ser Gln Glu Glu Gln  
 27437 300 305  
 E--> 27439 gttgacccgg tgtgttcttg tatagtcagt ggcacacgca cccgtcagcc  
 27440 ggccttttcc 1149  
 E--> 27441 ttcagggttcg tcaggctcac cggttctcac tgtgtctggg aagtaggact  
 27442 gatggtcatc 1209  
 E--> 27443 ttcattgacag gcggcatctc cactaagcct gtgtaactgt tccctctttg  
 27444 gttttcttag 1269  
 E--> 27445 cttttgaatt tgaagaagta cttttgaaga ctccattttt aagaaccgtg  
 27446 cagattttgc 1329  
 E--> 27447 taccaaaagt cttcaccact gtgttcttaa gtgaatgtta atttctgagg  
 27448 tttgggactt 1389  
 E--> 27449 tgtggtggtt tttttcttct tttcttttcc attcttcttt ctttcttttt  
 27450 atgttggttg 1449  
 E--> 27451 ctgtaaagtgc tgcacatcca gattgcatat caggacattg gttattttat  
 W--> 27452 GCTTTCTTGG 1509 ATATAACCAT GATCAGAGTG CCATGGC  
 E--> 27453 1536  
 27501 <210> SEQ ID NO: 170  
 27502 <211> LENGTH: 2560  
 27503 <212> TYPE: DNA  
 27504 <213> ORGANISM: Homo sapiens  
 W--> 27505 <220> FEATURE:  
 27506 <221> NAME/KEY: CDS *insert*  
 W--> 27507 ~~2227~~(202)..(1002)  
 W--> 27508 <400> SEQUENCE: 170  
 E--> 27509 ctggcctact ggggctccag ccgtgtcctg aggagctgga ccagccacat  
 27510 cccctggggc 60  
 E--> 27511 tgcagttgaa gcagaaccaa gtggccatcc cggcgttaga ccgtaggttc  
 27512 ctggteccgg 120  
 E--> 27513 agtggtcggg gcccgccagt gggcaggcag ctcttgetca caggccggcg  
 27514 tgcccaggcc 180  
 E--> 27515 gctggctctc cgcagggcgg a atg gcg ctg caa gtg gag ctg gta ccc acc  
 27516 231  
 27517 Met Ala Leu Gln Val Glu Leu Val Pro Thr  
 27518 1 5 10  
 E--> 27520 ggg gag atc atc cgc gtg gtt cat ccc cac agg ccc tgc aag ctt gcc  
 27521 279  
 27522 Gly Glu Ile Ile Arg Val Val His Pro His Arg Pro Cys Lys Leu Ala  
 27523 15 20 25  
 E--> 27525 ctg ggc agt gac ggg gtt cgg gtg acc atg gag agt gcg ctc acc gcc  
 27526 327  
 27527 Leu Gly Ser Asp Gly Val Arg Val Thr Met Glu Ser Ala Leu Thr Ala  
 27528 30 35 40  
 E--> 27530 cgt gac cgg gtg ggg gtg cag gat ttc gtg ctg ctg gag aac ttc acc

*same*

*see item 1  
 on  
 Enov  
 Summary  
 sheet*



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```

27531 375
27532 Arg Asp Arg Val Gly Val Gln Asp Phe Val Leu Leu Glu Asn Phe Thr
27533          45          50          55
E--> 27535 agc gag gcc gcc ttc atc ggg aac ctg cgg cgg cga ttt cgg gag aat
27536 423
27537 Ser Glu Ala Ala Phe Ile Gly Asn Leu Arg Arg Arg Phe Arg Glu Asn
27538          60          65          70
E--> 27540 ctc atc tac acc tac att ggc ccc gtc ctg gtc tct gtc aat ccc tac
27541 471
27542 Leu Ile Tyr Thr Tyr Ile Gly Pro Val Leu Val Ser Val Asn Pro Tyr
27543          75          80          85          90
E--> 27545 cgg gac ctg cag atc tac agc cgg cag cat atg gag cgt tac cgt ggc
27546 519
27547 Arg Asp Leu Gln Ile Tyr Ser Arg Gln His Met Glu Arg Tyr Arg Gly
27548          95          100          105
E--> 27550 gtc agc ttc tat gaa gtg ccc cct cac ctg ttt gcc gtg gcg gac act
27551 567
27552 Val Ser Phe Tyr Glu Val Pro Pro His Leu Phe Ala Val Ala Asp Thr
27553          110          115          120
E--> 27555 gtg tac cga gca ctg cgc acg gag cgt cgg gac cag gct gtg atg atc
27556 615
27557 Val Tyr Arg Ala Leu Arg Thr Glu Arg Arg Asp Gln Ala Val Met Ile
27558          125          130          135
E--> 27560 tct ggg gag agc ggg gca ggc aag acc gag gcc acc aag agg ctg ctg
27561 663
27562 Ser Gly Glu Ser Gly Ala Gly Lys Thr Glu Ala Thr Lys Arg Leu Leu
27563          140          145          150
E--> 27565 cag ttc tat gca gag acc tgc cca gcc ccc gag cgc gga ggt gcc gtg
27566 711
27567 Gln Phe Tyr Ala Glu Thr Cys Pro Ala Pro Glu Arg Gly Gly Ala Val
27568          155          160          165          170
E--> 27570 cgg gac cgg ctg cta cag agc aac ccg gtg ctg gag gcc ttt gga aat
27571 759
27572 Arg Asp Arg Leu Leu Gln Ser Asn Pro Val Leu Glu Ala Phe Gly Asn
27573          175          180          185
E--> 27575 gcc aag acc ctc cgg aac gat aac tcc agc agg ttc ggg aag tac atg
27576 807
27577 Ala Lys Thr Leu Arg Asn Asp Asn Ser Ser Arg Phe Gly Lys Tyr Met
27578          190          195          200
E--> 27580 gat gtg cag ttt gac ttc aag ggt gcc ccc gtg ggt ggc cac atc ctc
27581 855
27582 Asp Val Gln Phe Asp Phe Lys Gly Ala Pro Val Gly Gly His Ile Leu
27583          205          210          215
E--> 27585 agt tac ccc ctg gaa aag tca cga gtg gtg cac cag aat cat ggg gag
27586 903
27587 Ser Tyr Pro Leu Glu Lys Ser Arg Val Val His Gln Asn His Gly Glu
27588          220          225          230
E--> 27590 cgg aac ttc aca tct tct acc agc tgc tgg agg ggg gcg agg agg aga
27591 951

```

*same*

## RAW SEQUENCE LISTING

DATE: 04/24/2002

PATENT APPLICATION: US/10/089,320

TIME: 07:48:46

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\04242002\J089320.raw

27592 Arg Asn Phe Thr Ser Ser Thr Ser Cys Trp Arg Gly Ala Arg Arg Arg  
 27593 235 240 245 250  
 E--> 27595 ctc ttc gca ggc tgg gct tgg aac gga acc ccc aga gct atc tgt acc  
 27596 999  
 27597 Leu Phe Ala Gly Trp Ala Trp Asn Gly Thr Pro Arg Ala Ile Cys Thr  
 27598 255 260 265  
 E--> 27600 tgg tgaaggccag tgtgccaaag tcttcttcat caacgacaag agtgactgga  
 27601 aggtcg 1058  
 27602 Trp  
 E--> 27604 tcaggaagggc tctgacagtc attgatttca ccgaggatga agtggaggac  
 27605 ctgctgagca 1118  
 E--> 27606 tcgtggccag cgtccttcat ttgggcaaca tccactttgc tgccaacgag  
 27607 gagagcaatg 1178  
 E--> 27608 cccaggtcac caccgagaac cagctcaagt atctgagccc attcagtatg  
 27609 cgggtgcctgt 1238  
 E--> 27610 tgtgaaatac gaccgcaagg gctacaagcc tcgctcccg cagctgctgc  
 27611 tcacgcccac 1298  
 E--> 27612 cgccgtcgtc atcgtggagg acgcccaggt caagcagagg attgattacg  
 27613 ccaacctgac 1358  
 E--> 27614 cggaatctct gtcagcagcc tgagcgacag tctttttgtg cttcatgtac  
 27615 agcgtgcgga 1418  
 E--> 27616 caataagcaa aaggagatg tgggtgctgca gagtgaccac gtgattgaga  
 27617 cgctgaccaa 1478  
 E--> 27618 gacagccctc agtgccaacc gcgtgaacag catcaacatc aaccagggca  
 27619 gcatcacgtt 1538  
 E--> 27620 tgcagggggc cccggcagg atggcaccat tgacttcaca cccggctcgg  
 27621 agctgctcat 1598  
 E--> 27622 caccaaggcc aagaacgggc acctggctgt ggtcgcccca cggtgaatt  
 27623 ctggtgata 1658  
 E--> 27624 aaggcgccca ctggaccctc ccaacgccc atgctttgct tttctcctcc  
 27625 tccccttccc 1718  
 E--> 27626 agttacaaa gactcgaact tccagacagg gaccagggga cacccegaag  
 27627 cccacctgca 1778  
 E--> 27628 atctcccacc tctgcccac ccctctcttg agggagcagc aggggccagg  
 27629 agctaccca 1838  
 E--> 27630 ggagtggggc aggcggggc acagcaatag gaaagccagg gccagagcga  
 27631 gccatgccag 1898  
 E--> 27632 ccctactgcc gatgccaaat atttgagaga agggaacttt tgctgagggt  
 27633 ttctctgagg 1958  
 E--> 27634 ttttttttga tgetttatag gaaactattt tttaaaaaa gccatttccc  
 27635 acccaaggac 2018  
 E--> 27636 acagtggatg tgttttccct gactccagca gggcaaggaa atgtagccga  
 27637 gaggttggtg 2078  
 E--> 27638 gggctgggct ctggtgcctt cttccctggc caggacacct ctctcctga  
 27639 ttcccttggc 2138  
 E--> 27640 accttgtctt tctgtctgtt tacctgtctc cctgcctgcc catctgcatc  
 27641 ttttgagcc 2198  
 E--> 27642 cactctgact tccatctggg ggetgagacc acccttgcct gcccccttct  
 27643 ttctgcctta 2258

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/089,320

DATE: 04/24/2002

TIME: 07:48:46

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\04242002\J089320.raw

E--> 27644 agaattgtcct ttttaggtggt gcatgggtggc tcacgcctgt aaccccagca  
 27645 ctttgggagg 2318  
 E--> 27646 cggagacggg cagataacct gaggtcagga tttcgagacc aacctgacct  
 27647 acatggagaa 2378  
 E--> 27648 actccgcctc tggtaaggat acaaaattag ccgggcatgg tgggtgcacgc  
 27649 ctctaattccc 2438  
 E--> 27650 agctgctcgg gaggtctgagg caggagaatc acttgaacct gggaagtgga  
 27651 gggtgcagtg 2498  
 E--> 27652 agccaagagt acaccactgc actccagcct gggcaacaga gcgagactcc  
 27653 gtcttaaaaa 2558  
 27654 aa  
 27696 <210> SEQ ID NO: 172  
 27697 <211> LENGTH: 2650  
 27698 <212> TYPE: DNA  
 27699 <213> ORGANISM: Homo sapiens  
 W--> 27700 <220> FEATURE:  
 27701 <221> NAME/KEY: CDS  
 27702 <222> LOCATION: (116)..(1216)  
 W--> 27703 <400> SEQUENCE: 172  
 E--> 27704 cttttgtctgc tgcgcccggg caggggctgc cgcggcccca ggtcccgtt  
 27705 cgagacgcgg 60  
 E--> 27706 cgcgggtccag gcgggagggc actccctagg aagggaccgc ggcggggagg  
 27707 aggaa atg 118  
 27708  
 27709  
 E--> 27711 agg ccg cgc gga agg aag gcg gcg agc ccc ggg gcc ccg agg cct tgg  
 27712 166  
 27713 Arg Pro Arg Gly Arg Lys Ala Ala Ser Pro Gly Ala Pro Arg Pro Trp  
 27714 5 10 15  
 E--> 27716 ccg cgt cac agc acc cac atg gcc tct gga gtg ggc gcg gcc ttc gag  
 27717 214  
 27718 Pro Arg His Ser Thr His Met Ala Ser Gly Val Gly Ala Ala Phe Glu  
 27719 20 25 30  
 E--> 27721 gaa ctg cct cac gac ggc acg tgt gac gag tgc gag ccc gac gag gct  
 27722 262  
 27723 Glu Leu Pro His Asp Gly Thr Cys Asp Glu Cys Glu Pro Asp Glu Ala  
 27724 35 40 45  
 E--> 27726 ccg ggg gcc gag gaa gtg tgc cga gaa tgc ggc ttc tgc tac tgc cgc  
 27727 310  
 27728 Pro Gly Ala Glu Glu Val Cys Arg Glu Cys Gly Phe Cys Tyr Cys Arg  
 27729 50 55 60 65  
 E--> 27731 cgc cat gcc gag gcg cac agg cag aag ttc ctc agt cac cat ctg gcc  
 27732 358  
 27733 Arg His Ala Glu Ala His Arg Gln Lys Phe Leu Ser His His Leu Ala  
 27734 70 75 80  
 E--> 27736 gaa tac gtc cac ggc tcc cag gcc tgg acc ccg cca gct gac gga gag  
 27737 406  
 27738 Glu Tyr Val His Gly Ser Gln Ala Trp Thr Pro Pro Ala Asp Gly Glu  
 27739 85 90 95

2560

Met  
1

## RAW SEQUENCE LISTING

DATE: 04/24/2002

PATENT APPLICATION: US/10/089,320

TIME: 07:48:46

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\04242002\J089320.raw

```

E--> 27741 ggg gcg ggg aag gaa gaa gcg gag gtc aag gtg gag cag gag agg gag
      27742 454
      27743 Gly Ala Gly Lys Glu Glu Ala Glu Val Lys Val Glu Gln Glu Arg Glu
      27744 100 105 110
E--> 27746 ata gaa agc gag gca ggg gaa gag agt gag tcg gag gaa gag agc gag
      27747 502
      27748 Ile Glu Ser Glu Ala Gly Glu Glu Ser Glu Ser Glu Glu Glu Ser Glu
      27749 115 120 125
E--> 27751 tca gag gaa gag agc gag aca gag gaa gag agt gag gat gag agc gat
      27752 550
      27753 Ser Glu Glu Glu Ser Glu Thr Glu Glu Glu Ser Glu Asp Glu Ser Asp
      27754 130 135 140 145
E--> 27756 gag gag agt gaa gaa gac agc gag gaa gaa atg gag gat gag caa gaa
      27757 598
      27758 Glu Glu Ser Glu Glu Asp Ser Glu Glu Glu Met Glu Asp Glu Gln Glu
      27759 150 155 160
E--> 27761 agc gag gcc gaa gaa gac aac caa gaa gaa ggg gaa tcc gag gcg gag
      27762 646
      27763 Ser Glu Ala Glu Glu Asp Asn Gln Glu Glu Gly Glu Ser Glu Ala Glu
      27764 165 170 175
E--> 27766 gga gaa act gag gca gaa agt gaa ttt gac cca gaa ata gaa atg gaa
      27767 694
      27768 Gly Glu Thr Glu Ala Glu Ser Glu Phe Asp Pro Glu Ile Glu Met Glu
      27769 180 185 190
E--> 27771 gca gag aga gtg gcc aag agg aag tgt ccg gac cat ggg ctt gat ttg
      27772 742
      27773 Ala Glu Arg Val Ala Lys Arg Lys Cys Pro Asp His Gly Leu Asp Leu
      27774 195 200 205
E--> 27776 agt acc tat tgc cag gaa gat agg cag ctc atc tgt gtc ctg tgt cca
      27777 790
      27778 Ser Thr Tyr Cys Gln Glu Asp Arg Gln Leu Ile Cys Val Leu Cys Pro
      27779 210 215 220 225
E--> 27781 gtc att ggg gct cac cag ggc cac caa ctc tcc acc cta gac gaa gcc
      27782 838
      27783 Val Ile Gly Ala His Gln Gly His Gln Leu Ser Thr Leu Asp Glu Ala
      27784 230 235 240
E--> 27786 ttt gaa gaa tta aga agc aaa gac tca ggt gga ctg aag gcc gct atg
      27787 886
      27788 Phe Glu Glu Leu Arg Ser Lys Asp Ser Gly Gly Leu Lys Ala Ala Met
      27789 245 250 255
E--> 27791 atc gaa ttg gtg gaa agg ttg aag ttc aag agc tca gac cct aaa gta
      27792 934
      27793 Ile Glu Leu Val Glu Arg Leu Lys Phe Lys Ser Ser Asp Pro Lys Val
      27794 260 265 270
E--> 27796 act cgg gac caa atg aag atg ttt ata cag cag gaa ttt aag aaa gtt
      27797 982
      27798 Thr Arg Asp Gln Met Lys Met Phe Ile Gln Gln Glu Phe Lys Lys Val
      27799 275 280 285
E--> 27801 cag aaa gtg att gct gat gag gag cag aag gcc ctt cat cta gtg gac

```

## RAW SEQUENCE LISTING

DATE: 04/24/2002

PATENT APPLICATION: US/10/089,320

TIME: 07:48:46

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\04242002\J089320.raw

```

27802 1030
27803 Gln Lys Val Ile Ala Asp Glu Glu Gln Lys Ala Leu His Leu Val Asp
27804 290                295                300                305
E--> 27806 atc caa gag gca atg gcc aca gct cat gtg act gag ata ctg gca gac
27807 1078
27808 Ile Gln Glu Ala Met Ala Thr Ala His Val Thr Glu Ile Leu Ala Asp
27809                310                315                320
E--> 27811 atc caa tcc cac atg gat agg ttg atg act cag atg gcc caa gcc aag
27812 1126
27813 Ile Gln Ser His Met Asp Arg Leu Met Thr Gln Met Ala Gln Ala Lys
27814                325                330                335
E--> 27816 gaa caa ctt gat acc tct aat gaa tca gct gag cca aag gca gag ggc
27817 1174
27818 Glu Gln Leu Asp Thr Ser Asn Glu Ser Ala Glu Pro Lys Ala Glu Gly
27819                340                345                350
E--> 27821 gat gag gaa gga ccc agt ggt gcc agt gaa gaa gag gac aca
27822 tgaaggctt                1225
27823 Asp Glu Glu Gly Pro Ser Gly Ala Ser Glu Glu Glu Asp Thr
27824                355                360                365
E--> 27826 gctacccccca gtggaaaatc atccctccc cttgtgtgta tgtgacagcg
27827 tgtatgtaac                1285
E--> 27828 ggcttctgat ttctgtgaaa gctgctcagc aacaaacgta cttccaccag
27829 atgtgtcccc                1345
E--> 27830 agatccacag caggcacata tctctccaag ggatgaccag ttttatgctt
27831 actgtgtgct                1405
E--> 27832 tctcatcccc tggttgtggt aggtcaagga aaagagcccc tttgatccac
27833 caggagcaat                1465
E--> 27834 taagaaagggt ccttcaggta atccctcaat ggctgctttg aacttactca
27835 ggaaagccag                1525
E--> 27836 ccccccataat attgtattac caaacagtat cgctttgtta ggaaggatct
27837 ggaataatct                1585
E--> 27838 tgaagggaag tcagagtttt ctccctgcct attaacaaaa acccaatttt
27839 gttcatattg                1645
E--> 27840 aagcatgaaa taaatgagag caaggtaggg ccaaattaac tcttgtggac
27841 agtccctaaa                1705
E--> 27842 agtccagttc tacatttgtg aaaattgtgg tgccatgaat taagatggat
27843 gactggaaaa                1765
E--> 27844 aggtgttgga gaaagagtta aagatgagga agagatatatt ttagtatatg
27845 aagttatcca                1825
E--> 27846 ggacttgata ttcataattc agtgctgtgg aatgaaaaa aatgattgaa
27847 gaggtggaac                1885
E--> 27848 ggaaatgacc ttagggggaa aaaaaaggac caaagaagtc tgattaaaag
27849 ttgaaatcag                1945
E--> 27850 tatttctgaa ttcaaattgc ttgaatttcc aaaatagtca gttaaaggatc
27851 taatagaacc                2005
E--> 27852 agaattatatt ggggtgaattc tgcaggtttt atgggcttgt cacaacgtga
27853 agggctggaa                2065
E--> 27854 tgtatattac caaatgggaa ttteccattgt aggtttttgc tagtcccacc
27855 cccattttag                2125

```

## RAW SEQUENCE LISTING

DATE: 04/24/2002

PATENT APPLICATION: US/10/089,320

TIME: 07:48:46

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\04242002\J089320.raw

E--> 27856 cctaatttgg cttaaagcga gtatggggag aattgttccc attccatgtg  
 27857 ttctgaattc 2185  
 E--> 27858 agctcatctc ccagcatata gatatactct cctttaacte cgaccagaac  
 27859 ccttcttctc 2245  
 E--> 27860 gtggcactcc ccacccatag accttcagat catctccac accctggatc  
 27861 tcactctcct 2305  
 E--> 27862 cttagtaaca gagacactcc tgaggttggga cttccttgct tttctctact  
 27863 tccaaatcac 2365  
 E--> 27864 aatttcttac aaccaagctt tgtgctcccg agtaagcagg gatgtactag  
 27865 gggaatgtaa 2425  
 E--> 27866 aactgcaaac ttaaaaacct gcatcttctt gaagcatcag ttttacttac  
 27867 caaatggttt 2485  
 E--> 27868 agagtcataa gatgacctat ttttatataa aagttatatt atagaataaa  
 27869 atgttcatac 2545

E--&gt; 27870 gcatagactg ttaag

2560

27872 &lt;210&gt; SEQ ID NO: 173

27873 &lt;211&gt; LENGTH: 367

27874 &lt;212&gt; TYPE: PRT

27875 &lt;213&gt; ORGANISM: Homo sapiens

W--&gt; 27876 173

E--&gt; 27877 &lt;400&gt;

add <400> and move 173 down to <400> line

27877 Met Arg Pro Arg Gly Arg Lys Ala Ala Ser Pro Gly Ala Pro Arg Pro  
 27878 1 5 10 15  
 27879 Trp Pro Arg His Ser Thr His Met Ala Ser Gly Val Gly Ala Ala Phe  
 27880 20 25 30  
 27881 Glu Glu Leu Pro His Asp Gly Thr Cys Asp Glu Cys Glu Pro Asp Glu  
 27882 35 40 45  
 27883 Ala Pro Gly Ala Glu Glu Val Cys Arg Glu Cys Gly Phe Cys Tyr Cys  
 27884 50 55 60  
 27885 Arg Arg His Ala Glu Ala His Arg Gln Lys Phe Leu Ser His His Leu  
 27886 65 70 75 80  
 27887 Ala Glu Tyr Val His Gly Ser Gln Ala Trp Thr Pro Pro Ala Asp Gly  
 27888 85 90 95  
 27889 Glu Gly Ala Gly Lys Glu Glu Ala Glu Val Lys Val Glu Gln Glu Arg  
 27890 100 105 110  
 27891 Glu Ile Glu Ser Glu Ala Gly Glu Glu Ser Glu Ser Glu Glu Ser  
 27892 115 120 125  
 27893 Glu Ser Glu Glu Glu Ser Glu Thr Glu Glu Glu Ser Glu Asp Glu Ser  
 27894 130 135 140  
 27895 Asp Glu Glu Ser Glu Glu Asp Ser Glu Glu Glu Met Glu Asp Glu Gln  
 27896 145 150 155 160  
 27897 Glu Ser Glu Ala Glu Glu Asp Asn Gln Glu Glu Gly Glu Ser Glu Ala  
 27898 165 170 175  
 27899 Glu Gly Glu Thr Glu Ala Glu Ser Glu Phe Asp Pro Glu Ile Glu Met  
 27900 180 185 190  
 27901 Glu Ala Glu Arg Val Ala Lys Arg Lys Cys Pro Asp His Gly Leu Asp  
 27902 195 200 205  
 27903 Leu Ser Thr Tyr Cys Gln Glu Asp Arg Gln Leu Ile Cys Val Leu Cys  
 27904 210 215 220

## RAW SEQUENCE LISTING

DATE: 04/24/2002

PATENT APPLICATION: US/10/089,320

TIME: 07:48:46

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\04242002\J089320.raw

27905 Pro Val Ile Gly Ala His Gln Gly His Gln Leu Ser Thr Leu Asp Glu  
 27906 225 230 235 240  
 27907 Ala Phe Glu Glu Leu Arg Ser Lys Asp Ser Gly Gly Leu Lys Ala Ala  
 27908 245 250 255  
 27909 Met Ile Glu Leu Val Glu Arg Leu Lys Phe Lys Ser Ser Asp Pro Lys  
 27910 260 265 270  
 27911 Val Thr Arg Asp Gln Met Lys Met Phe Ile Gln Gln Glu Phe Lys Lys  
 27912 275 280 285  
 27913 Val Gln Lys Val Ile Ala Asp Glu Glu Gln Lys Ala Leu His Leu Val  
 27914 290 295 300  
 27915 Asp Ile Gln Glu Ala Met Ala Thr Ala His Val Thr Glu Ile Leu Ala  
 27916 305 310 315 320  
 27917 Asp Ile Gln Ser His Met Asp Arg Leu Met Thr Gln Met Ala Gln Ala  
 E--> 27918 325 325 330 330 335 335  
 27919 Lys Glu Gln Leu Asp Thr Ser Asn Glu Ser Ala Glu Pro Lys Ala Glu  
 E--> 27920 340 340 345 345 350 350  
 27921 Gly Asp Glu Glu Gly Pro Ser Gly Ala Ser Glu Glu Glu Asp Thr  
 E--> 27922 355 360 365  
 27934 <210> SEQ ID NO: 175  
 27935 <211> LENGTH: 29  
 27936 <212> TYPE: DNA  
 27937 <213> ORGANISM: Artificial Sequence  
 W--> 27938 <220> FEATURE:  
 27939 <223> OTHER INFORMATION: Description of the artificial sequence: a synthetic DNA  
 27941 <400> SEQUENCE: 175  
 E--> 27942 gtatcgattt aattgcgatc ccccatcag  
 E--> 27944 176 <210> ← insert <210> and insert 176  
 27945 <211> LENGTH: 24  
 27946 <212> TYPE: DNA  
 27947 <213> ORGANISM: Artificial Sequence  
 W--> 27948 <220> FEATURE:  
 27949 <223> OTHER INFORMATION: Description of the artificial sequence: a synthetic DNA  
 OK> 27951 <400> SEQUENCE: 176  
 E--> 27952 cacctactgtatgacacacattc 24  
 OK> 27954 <210> SEQ ID NO: 177

*misaligned  
 amino acid  
 has - see  
 item 3 on  
 Error Summary  
 sheet*

*delete  
 @29*

*insert a space between each group of 10 bases*  
 ↓  
*same error  
 in seq 177-181*

16

VARIABLE LOCATION SUMMARY

DATE: 04/24/2002

PATENT APPLICATION: US/10/089,320

TIME: 07:48:47

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\04242002\J089320.raw

Use of n's or Xaa's(NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:15; N Pos. 1503,1512,1538,1539,1544,1548,1559,1560,1564,1610,1611,1697  
Seq#:15; N Pos. 1698,1706,1707,1735,1750,1780,1781,1804,1805,1807,1809,1813  
Seq#:15; N Pos. 2317,2534,2726,2729,2746,2751,2785,2788,2797,2801,2813,2816  
Seq#:15; N Pos. 2827,2828,2859,2863,2864  
Seq#:67; N Pos. 1485  
Seq#:109; Xaa Pos. 49,65  
Seq#:110; Xaa Pos. 49,65  
Seq#:113; Xaa Pos. 17,18,19,31,34,35,109  
Seq#:114; Xaa Pos. 17,18,19,31,34,35,109  
Seq#:116; N Pos. 134,135  
Seq#:117; N Pos. 37  
Seq#:117; Xaa Pos. 4  
Seq#:118; Xaa Pos. 4  
Seq#:121; N Pos. 28  
Seq#:121; Xaa Pos. 9  
Seq#:122; Xaa Pos. 9  
Seq#:123; Xaa Pos. 59  
Seq#:124; Xaa Pos. 59  
Seq#:131; N Pos. 415,472  
Seq#:132; N Pos. 223,237,380,468  
Seq#:133; N Pos. 313



10/09, 320

17

aggggatcct gctgcttngc tttcttncct cgctacttcc taaaaagcaa cchaaagnt 1545  
 ttatgaatg ctannagant gttgcattgt gtatactgag ataactctgag gcatggagag 1605  
 caganncagg gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gtatgtgcgt gtgcgtgcac 1665  
 atgtgtgcct gcgtgttggt ataggacttt annctcctt nnggcatagg gaagtcacga 1725  
 aggattgctn gacatcagga gactnngggg ggattgtagc agacgtctgg gcttnncccc 1785  
 acccagagaa tagcccccnn onanacanat cagctggatt tacaaaagct tcaaagtctt 1845  
 ggtctgtgag tcaactcttca gtttggggagc tgggtctgtg gctttgatca gaaggtactt 1905  
 tcaaaagagg gctttccagg gctcagctcc caaccagctg ttaggacccc acccttttgc 1965  
 ctttattgtc gacgtgactc accagacgtc ggggagagag agcagtcaga ccgagctttt 2025  
 ctgctaacat ggggagggtg gcagacactg gcatagcacg gtagtggttt gggggagggt 2085  
 ttccgcaggt ctgctcccca cccctgcctc ggaagaataa agagaatgta gttccctact 2145  
 caggctttcg tagtgattag cttactaagg aactgaaaat gggccccttg tacaagctga 2205  
 gctgccccgg agggagggtg gagttccctg ggcttctggc acctgtttct aggcctaacc 2265  
 attagtactt actgtgcagg gaaccaaacc aaggtctgag aaatgcggac ancccgagcg 2325  
 agcaccocaa agtgcacaaa gctgagtaaa aagctgcccc cttcaaacag aactagactc 2385  
 agttttcaat tccatcctaa aactcctttt aaccaagctt agcttctcaa agggctaacc 2445  
 aagccttgga accgccagat cttttctgta ggctaattcc tcttggccaa cggcatatgg 2505  
 agtgtcotta ttgctaaaaa ggattccgnc tccttcaaag aagttttatt tttggtocag 2565  
 agtacttggt ttcccgatgt gtccagccag ctccgcagca gcttttcaaa atgcactatg 2625  
 cctgattgct gatcgtgttt taacttttct ttttctggt tttattttgg tattaagtcg 2685  
 ctggctttat ttgtaaagct gttataaata tatattatat naantatatt aaaaaggaaa 2745  
 ntgttncaga tgtttatttg tataattact tgattcacan agnagaaaa antgamtgta 2805  
 ttctctgttt ngaagagaag annaattttt ttttctcta gggagaggta cagnttntnt 2865

see  
 item 9  
 on Encl  
 Summary  
 Sheet

Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

<210> 159

<211> 20

<212> DNA

<220>

→ <213> ← insert this mandatory numeric identifier  
and response

<223> Description of the artificial sequence: an artificially synthesized primer sequence

(same env in Seqs. 160 and 161)

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/089,320

DATE: 04/24/2002

TIME: 07:48:47

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\04242002\J089320.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number  
 L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:1462 M:252 E: No. of Seq. differs, <211> LENGTH:Input:2433 Found:2423 SEQ:7  
 L:2902 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15  
 L:2902 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:1485  
 L:2904 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15  
 L:2904 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:1545  
 L:2906 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15  
 L:2906 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:1605  
 L:2908 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15  
 L:2908 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:1665  
 L:2910 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15  
 L:2910 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:1725  
 L:2912 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15  
 L:2912 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:1785  
 L:2928 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15  
 L:2928 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:2265  
 L:2936 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15  
 L:2936 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:2505  
 L:2942 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15  
 L:2942 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:2685  
 L:2944 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15  
 L:2944 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:2745  
 L:2946 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15  
 L:2946 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:2805  
 L:13964 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:67  
 L:13964 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67 after pos.:1457  
 L:17641 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:88  
 L:18375 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:94  
 L:21052 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:109  
 L:21052 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:109 after pos.:435  
 L:21058 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:109  
 L:21058 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:109 after pos.:483  
 L:21313 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:110  
 M:340 Repeated in SeqNo=110  
 L:21766 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:113 after pos.:96  
 L:21772 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:113 after pos.:144  
 L:21796 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:113 after pos.:336  
 L:21929 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:114 after pos.:16  
 L:21933 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:114 after pos.:32  
 L:21949 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:114 after pos.:96  
 L:22033 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:116 after pos.:120  
 L:22076 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:117 after pos.:0  
 L:22078 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:117 after pos.:52  
 L:22147 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:118 after pos.:0  
 L:22410 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:121 after pos.:0  
 L:22412 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:121 after pos.:49  
 L:22515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:122 after pos.:0

VERIFICATION SUMMARY

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Input Set : A:\PTO.AMC.txt

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L:22610 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:123 after pos.:370  
 L:22653 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:124 after pos.:48  
 L:23187 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:131 after pos.:360  
 L:23191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:131 after pos.:420  
 L:23301 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:132 after pos.:180  
 L:23313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:132 after pos.:360  
 L:23317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:132 after pos.:420  
 L:23379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:133 after pos.:300  
 L:27235 M:282 W: Numeric Field Identifier Missing, <213> is required.  
 L:27252 M:282 W: Numeric Field Identifier Missing, <213> is required.  
 L:27269 M:282 W: Numeric Field Identifier Missing, <213> is required.  
 L:27277 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:27279 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:27286 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:27288 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:27295 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:27297 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:27304 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:27306 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:27313 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:27315 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:27322 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:27324 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:27331 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:27334 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:27335 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:168  
 L:27335 M:112 C: (48) String data converted to lower case,  
 M:112 Repeated in SeqNo=168  
 M:254 Repeated in SeqNo=168  
 L:27452 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:5  
 L:27453 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:168  
 L:27453 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1536 Found:1499 SEQ:168  
 L:27459 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:27505 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:27507 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:170  
 L:27508 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:27509 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:170  
 M:112 Repeated in SeqNo=170  
 M:254 Repeated in SeqNo=170  
 L:27660 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:27700 M:283 W: Missing Blank Line separator, <220> field identifier  
 L:27703 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:27704 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:172  
 M:112 Repeated in SeqNo=172  
 M:254 Repeated in SeqNo=172  
 L:27870 M:252 E: No. of Seq. differs, <211> LENGTH:Input:2650 Found:2560 SEQ:172  
 L:27876 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:  
 L:27877 M:200 E: Mandatory Header Field missing, <400> is required.  
 L:27918 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0

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M:332 Repeated in SeqNo=173

L:27928 M:283 W: Missing Blank Line separator, <220> field identifier

L:27938 M:283 W: Missing Blank Line separator, <220> field identifier

L:27942 M:254 E: No. of Bases conflict, LENGTH:Input:29 Counted:31 SEQ:175

L:27942 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2

M:254 Repeated in SeqNo=175

L:27944 M:252 E: No. of Seq. differs, <211> LENGTH:Input:29 Found:31 SEQ:175

L:27948 M:283 W: Missing Blank Line separator, <220> field identifier

L:27951 M:282 W: Numeric Field Identifier Missing, <210> is required.

L:27951 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:175 differs:176

L:27954 M:214 E: (33) Seq.# missing, SEQ ID NO:176

L:27958 M:283 W: Missing Blank Line separator, <220> field identifier

L:27968 M:283 W: Missing Blank Line separator, <220> field identifier

L:27978 M:283 W: Missing Blank Line separator, <220> field identifier

L:27988 M:283 W: Missing Blank Line separator, <220> field identifier

L:27998 M:283 W: Missing Blank Line separator, <220> field identifier

L:18 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (181) Counted (180)